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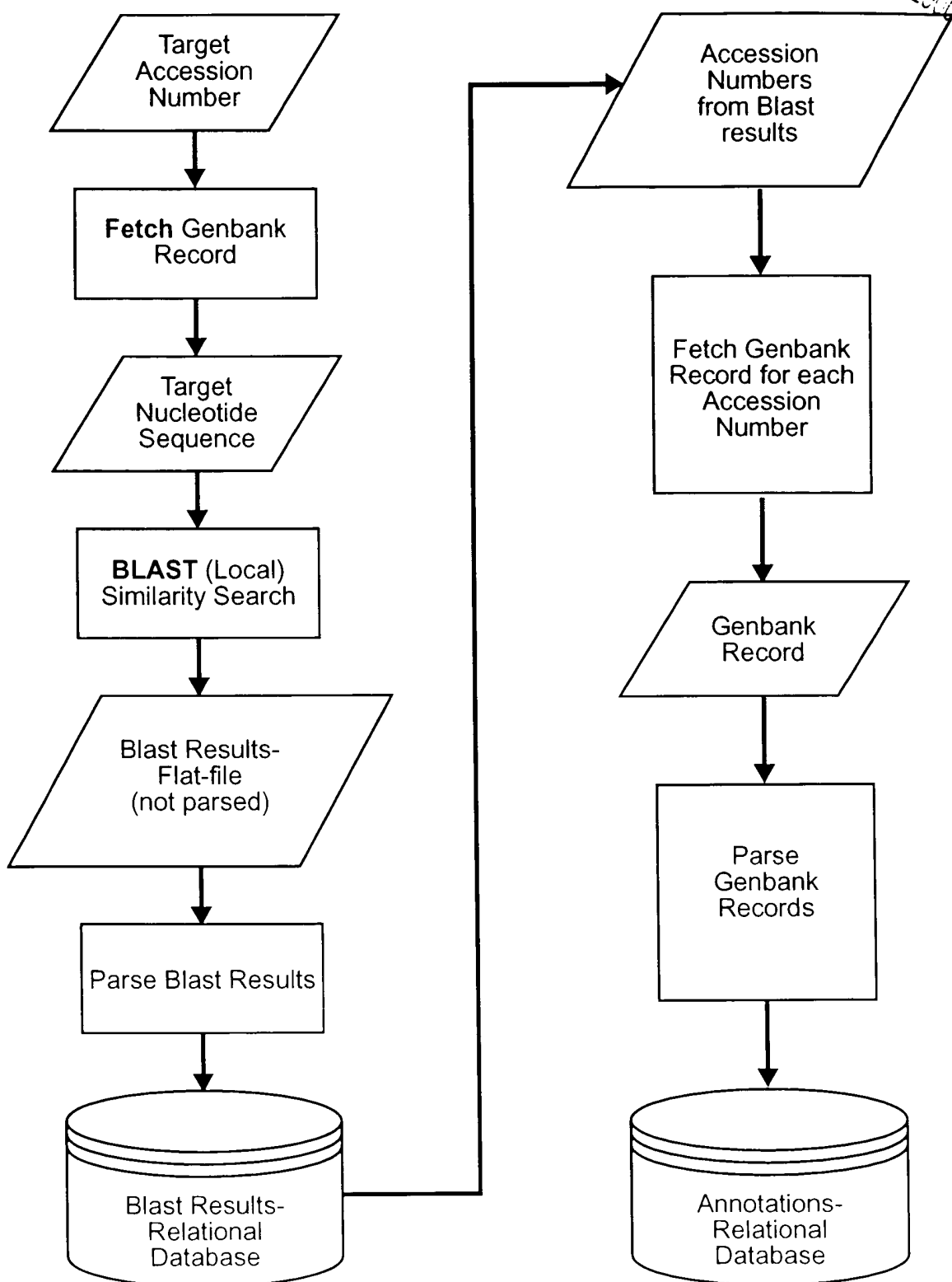


Figure 3



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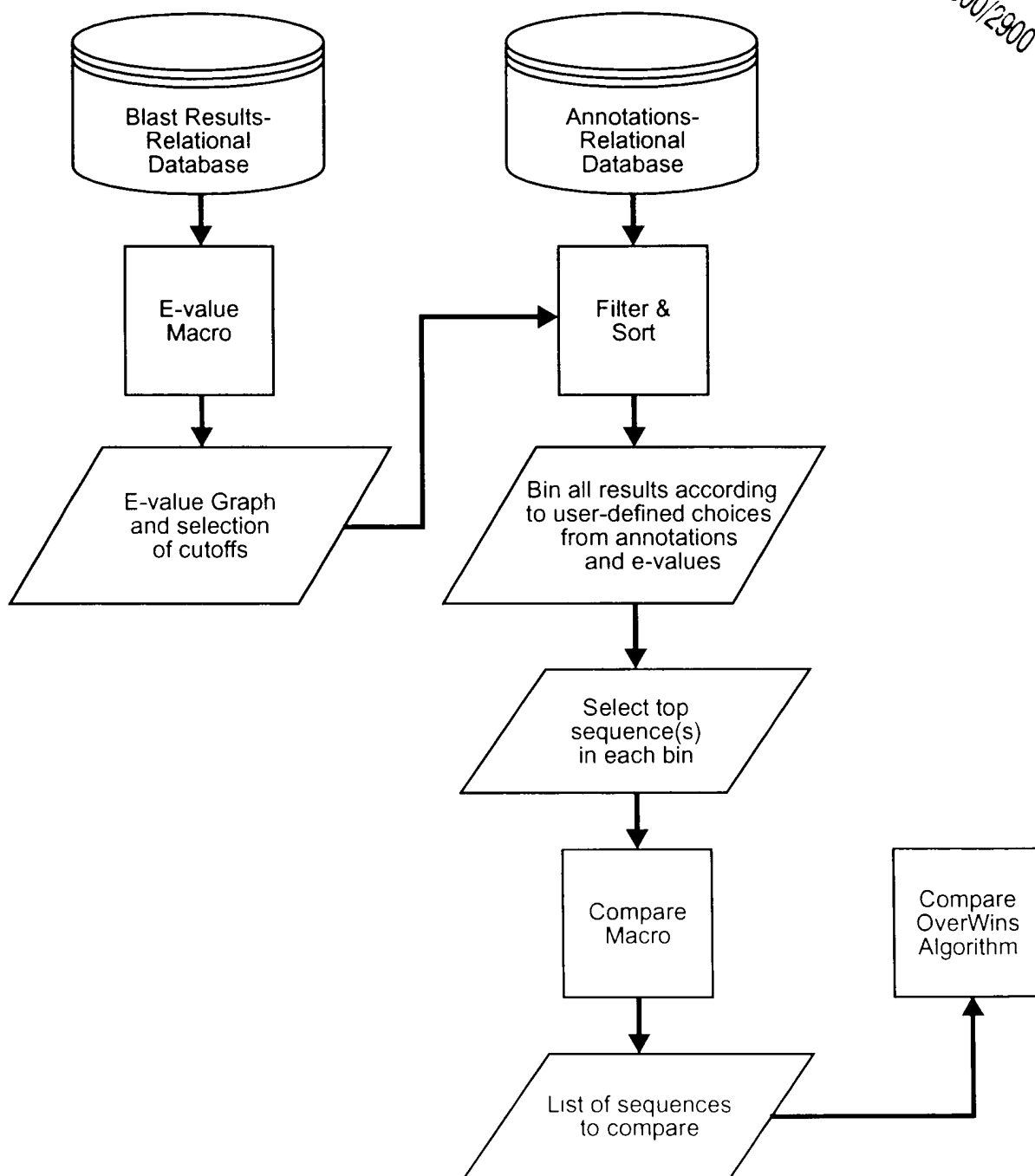
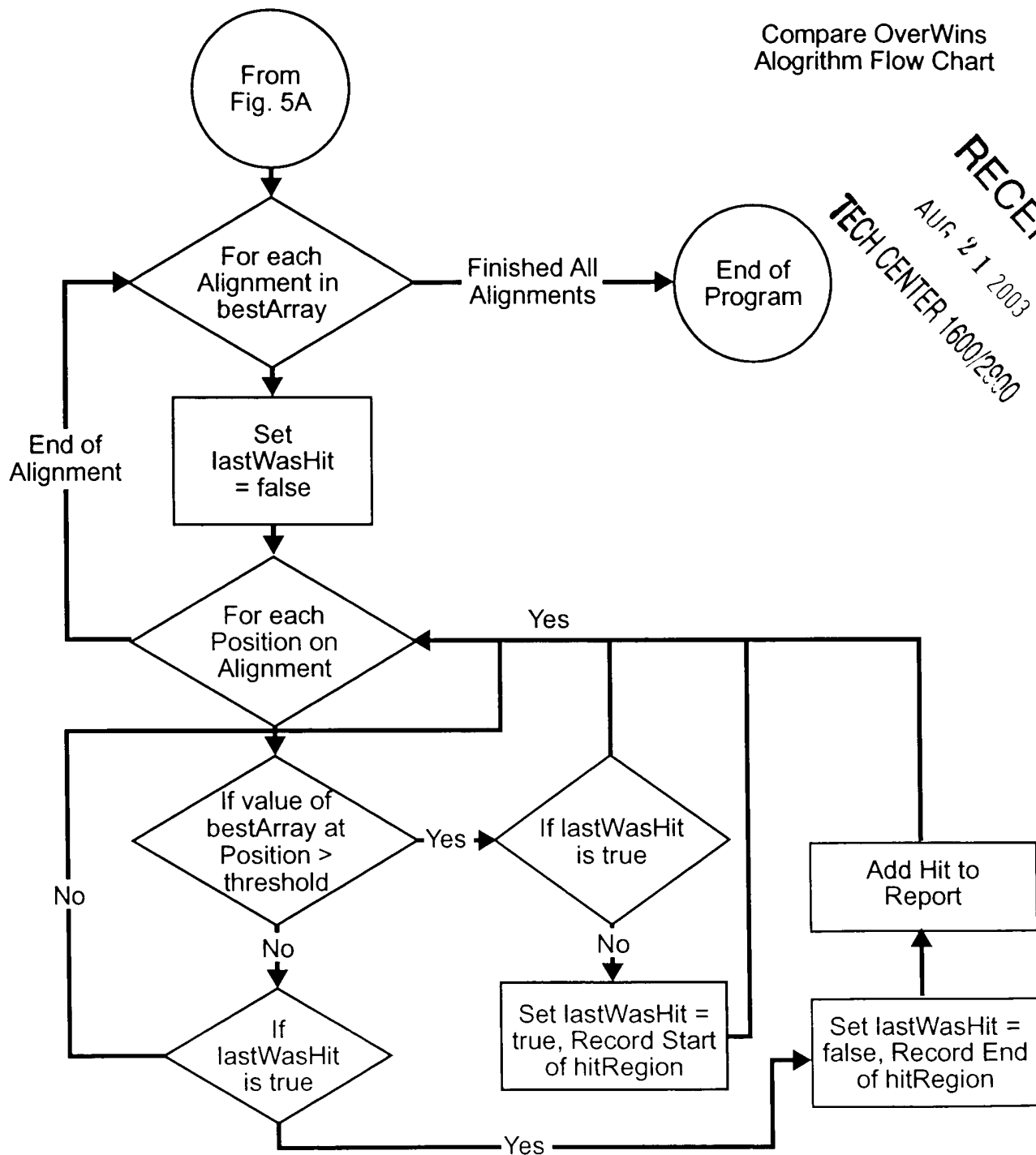


Figure 4



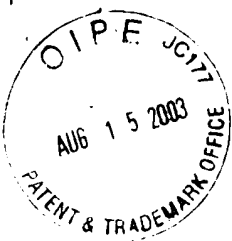
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Compare OverWins
Algorithm Flow Chart



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Figure 5B



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Input:
Sequence A length a
Sequence B length b
Window Size

Output:
Array of size a by b of unsigned chars (0-255)
Each point represents the number of matches in the
window at that alignment and position

Compare OverWins
Algorithm Flow Chart
Basic Compare

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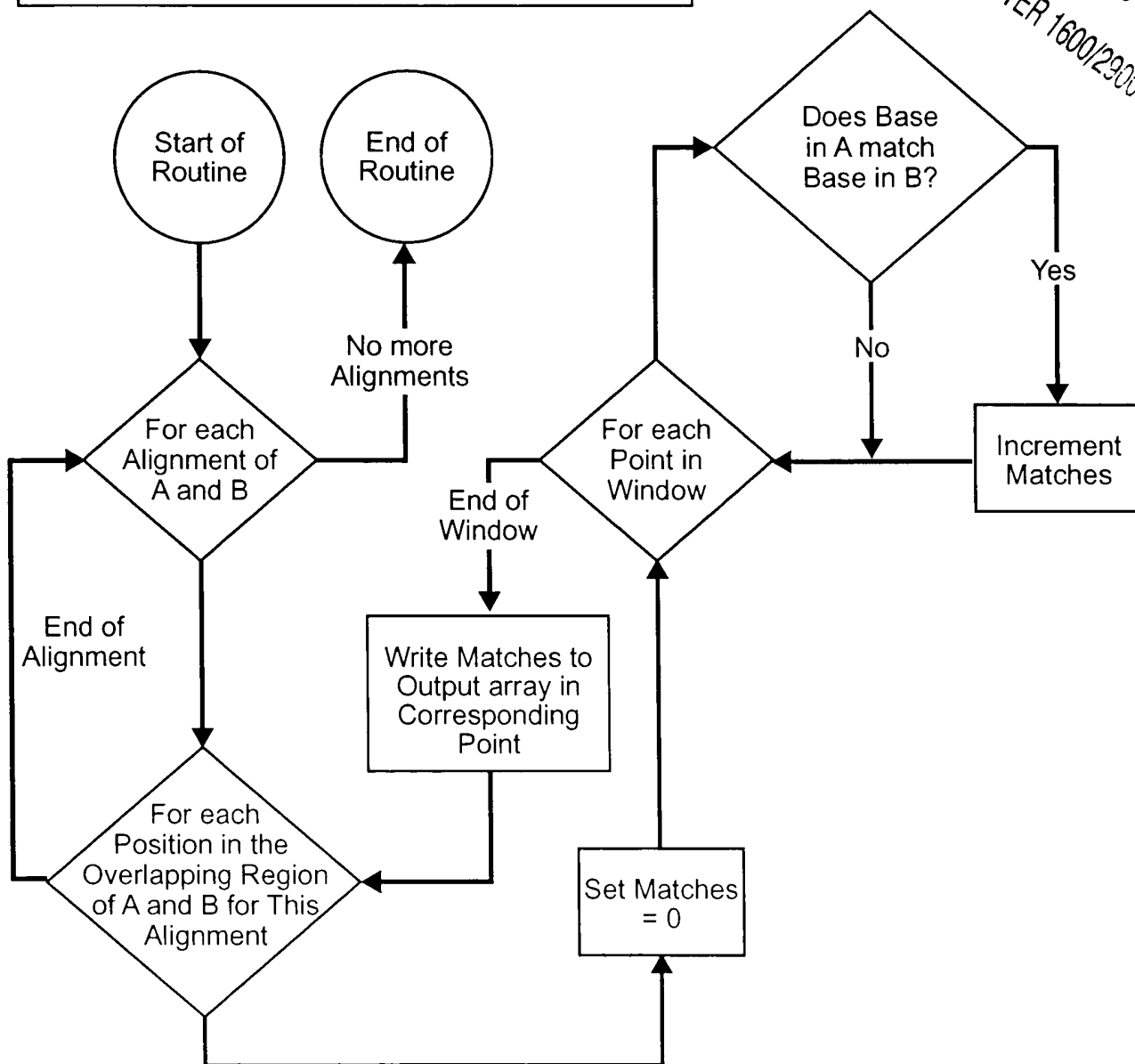
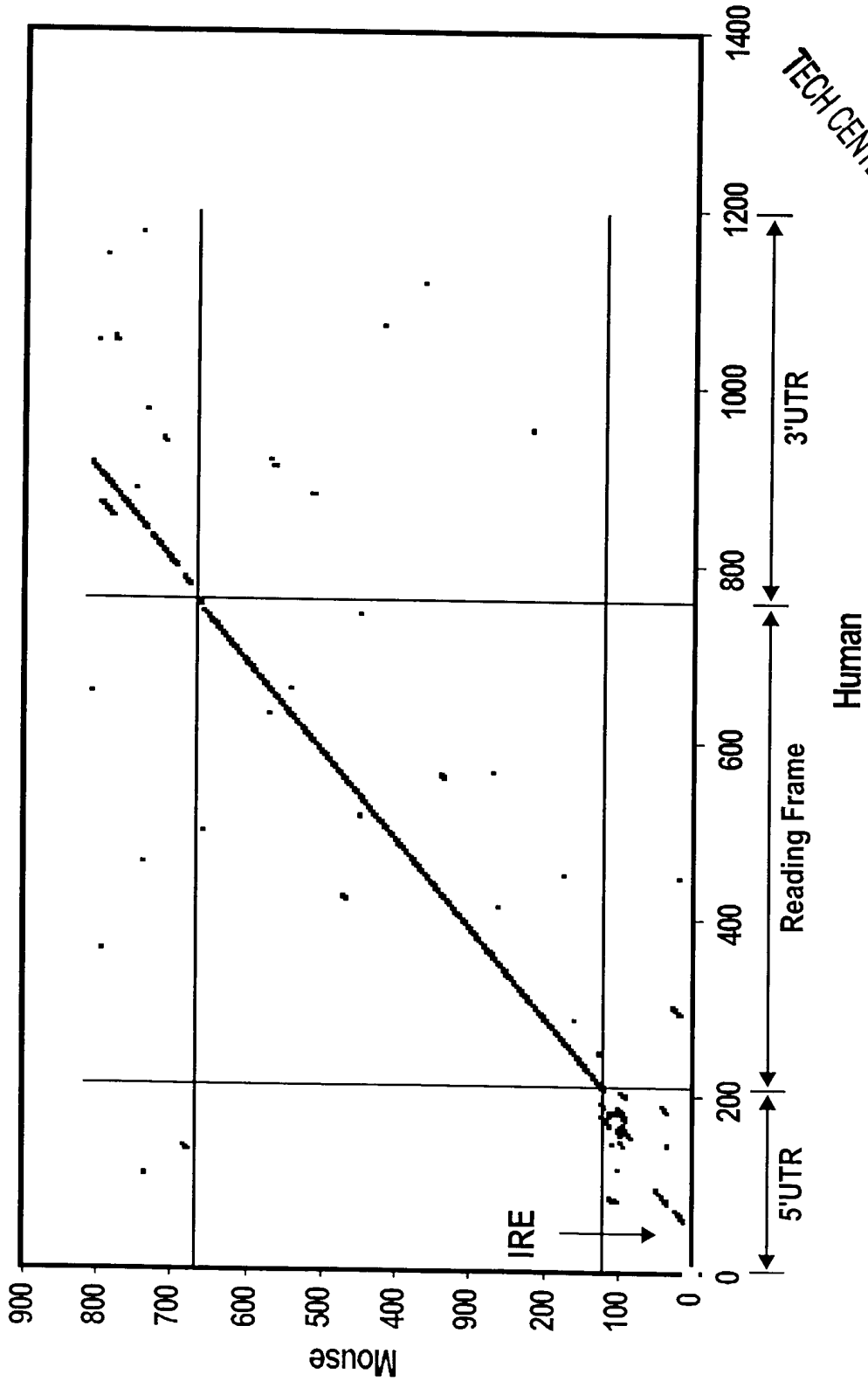


Figure 5C



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Figure 6



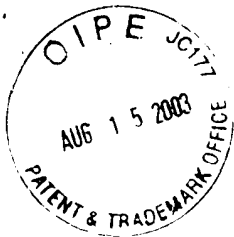
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Self Complementation Analysis - Single Sequence

3'	G	A	C	G	A	A	G	U	U	G	C	A	C	G	A	A	C	C	U	A	C	C	5'
23																							
22	*	&		*		*																	
21		&	*		*		*																
20			*		*		*																
19				*	*		*																
18				*	*		*																
17				*	*		*																
16						*	*																
15						*	*																
14						*	*																
13						*	*																
12						*	*																
11						*	*																
10						*	*																
9						*	*																
8						*	*																
7						*	*																
6						*	*																
5						*	*																
4						*	*																
3						*	*																
2						*	*																
1						*	*																
5'	C	U	G	C	U	C	A	A	C	A	G	U	G	U	G	C	U	G	A	U	G	U	C

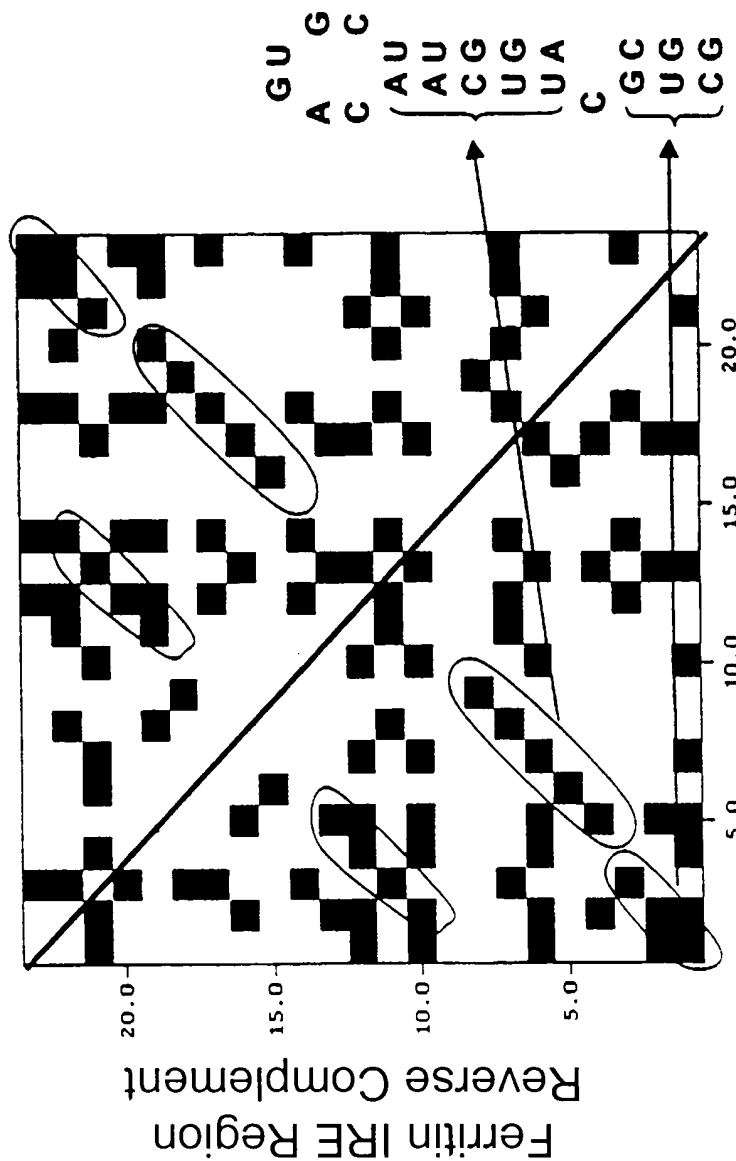
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Figure 7



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Self Complementarity Comparisons
13 ortholog overlay



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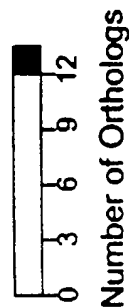
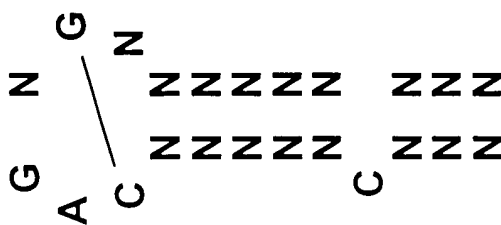


Figure 8



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IRE
 Stem-loop Model

IRE String descriptor

This descriptor allows for

- a wobble (W) of 2
- no mismatches
- N can be any nucleotide
- H refers to the stem region
- S refers to the single stranded region

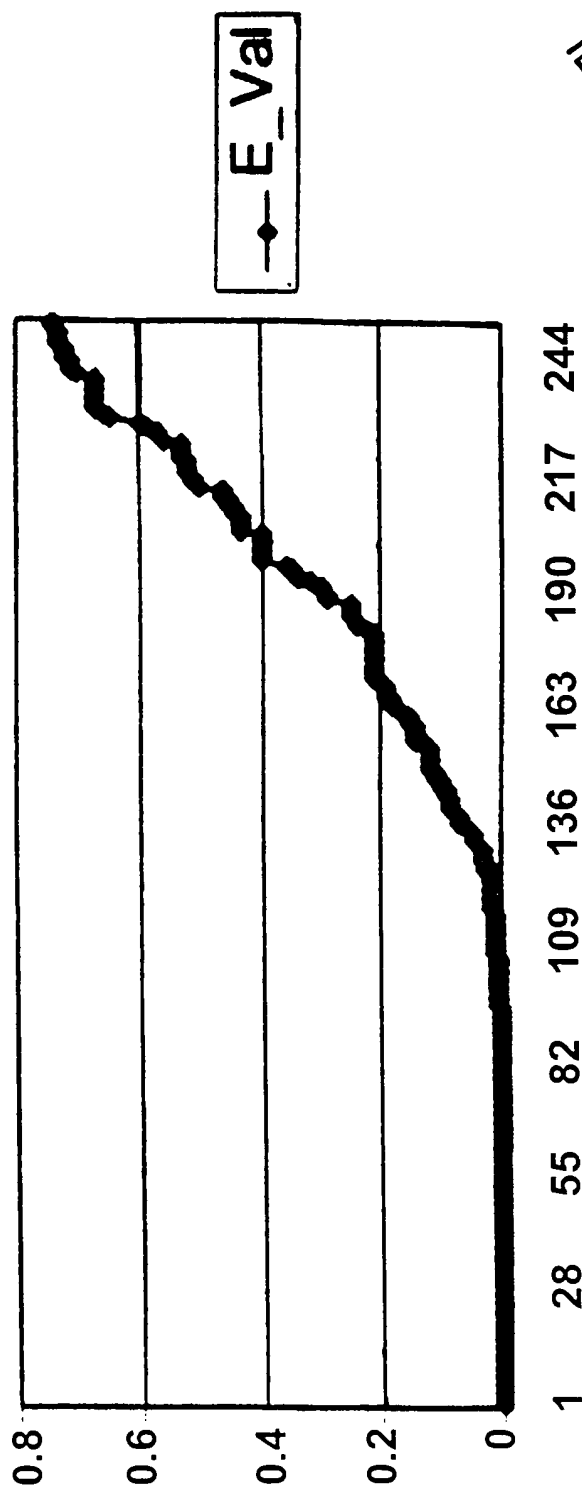
H1	S1	H2	S2	H2	H1
H1	3:3	NNN:NNN			
S1	1	C			
H2	5:5	NNNNN:NNNNN			
S2	6	CAGNGN			
W2					
M0					

Figure 9



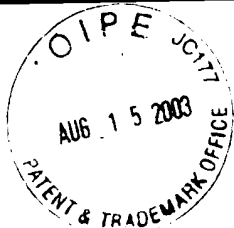
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E-Val



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Figure 10



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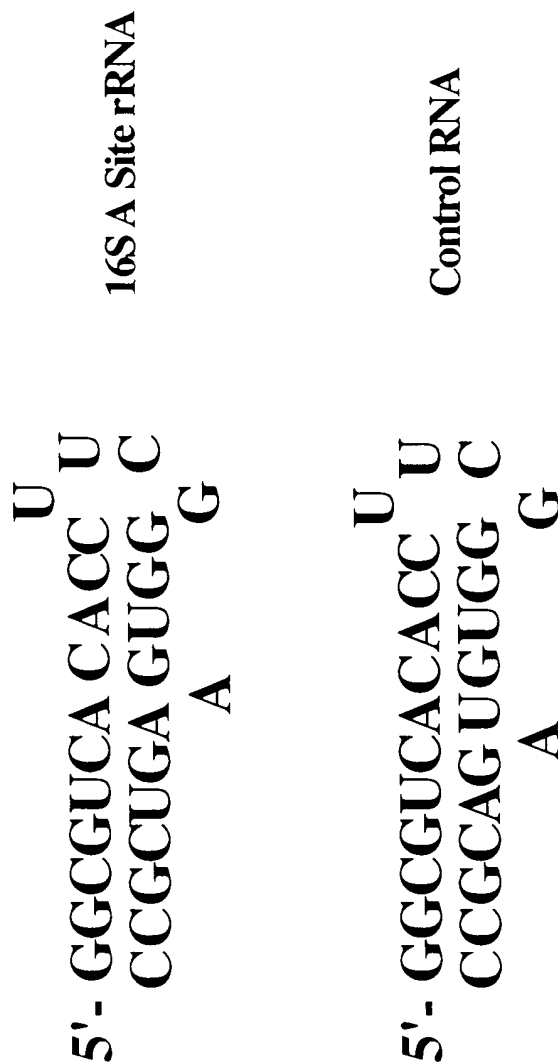
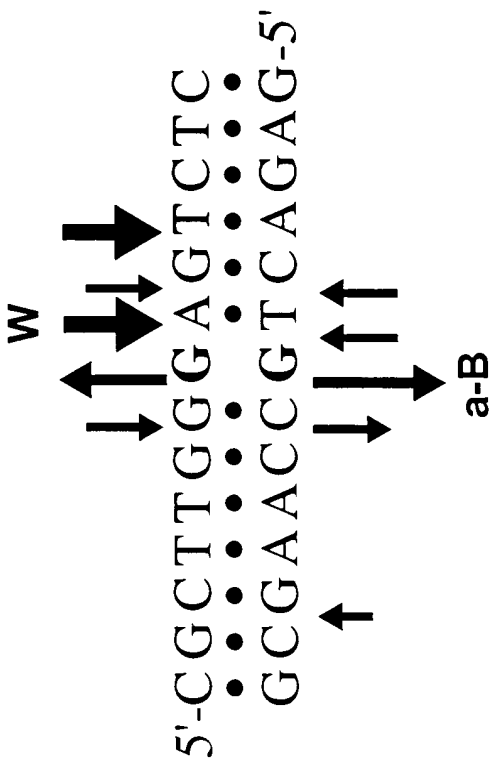


Figure 40

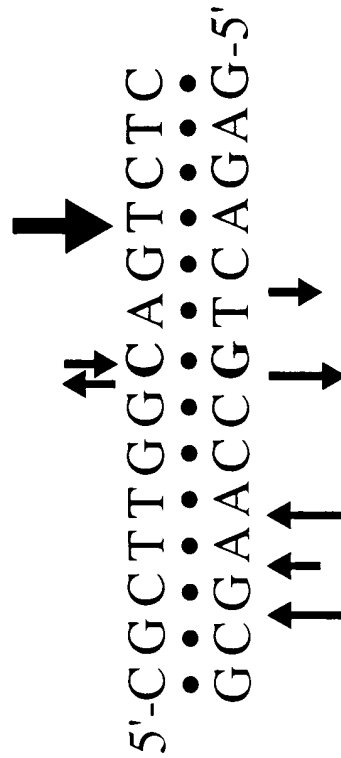


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A.



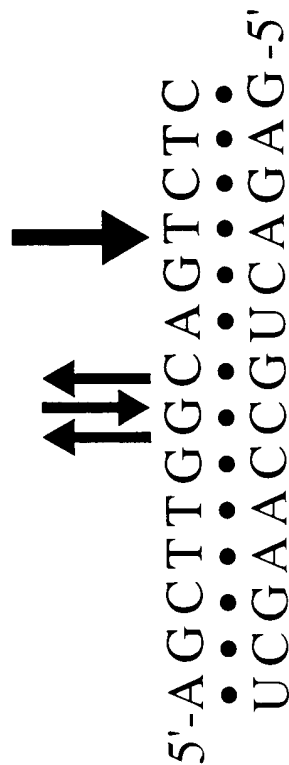
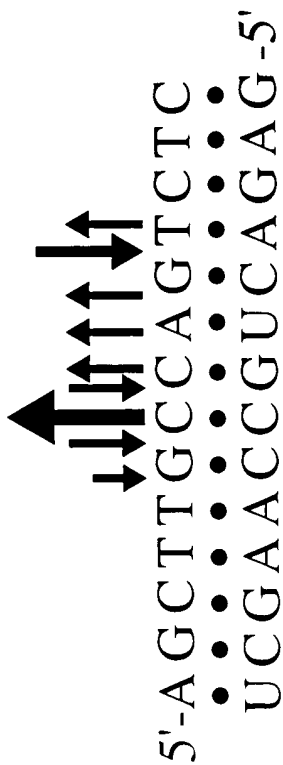
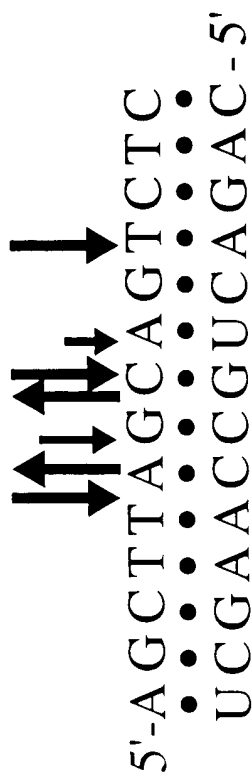
B.

Figure 47



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MS Fragmentation of DNA:RNA duplexes

Figure 48



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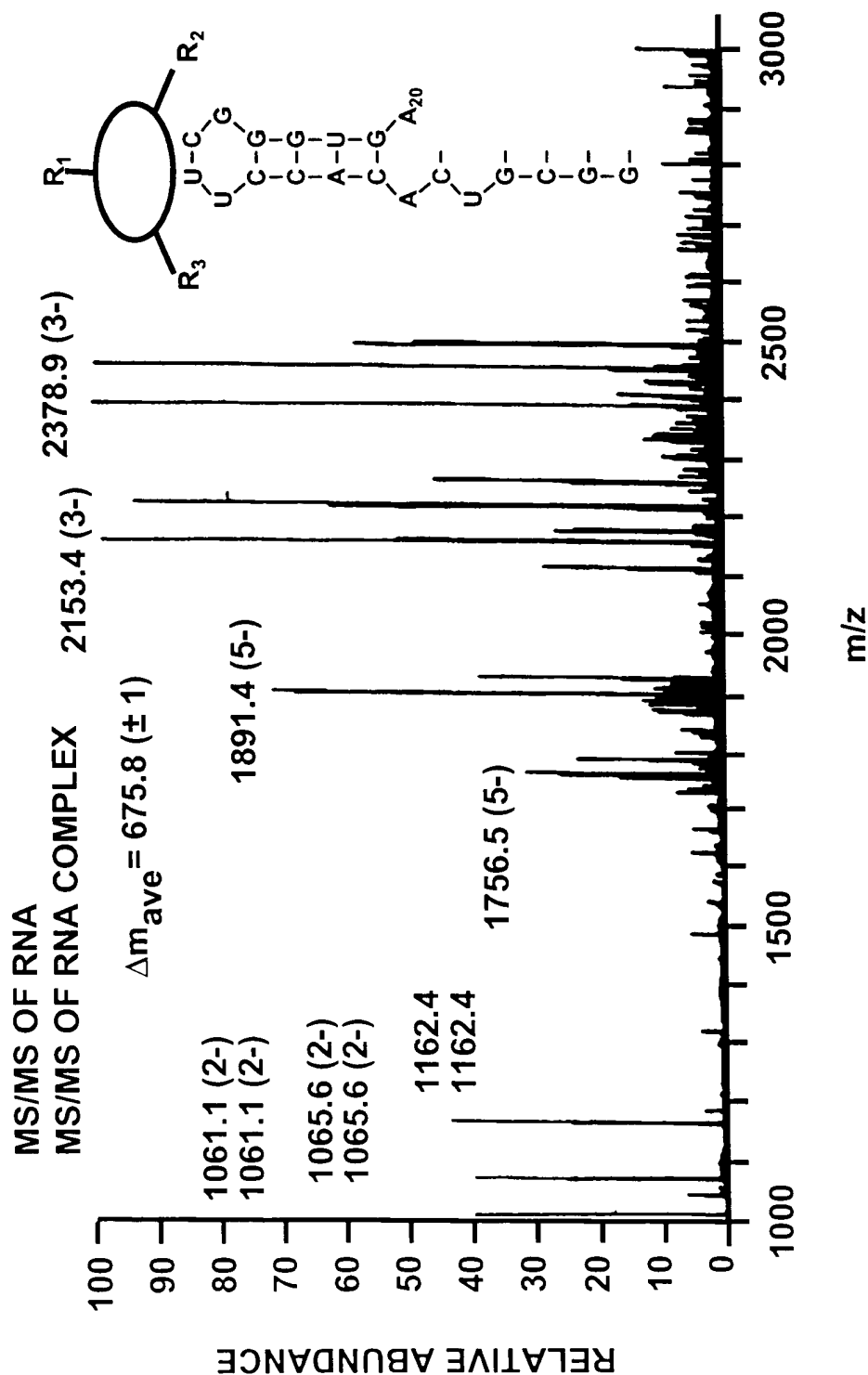
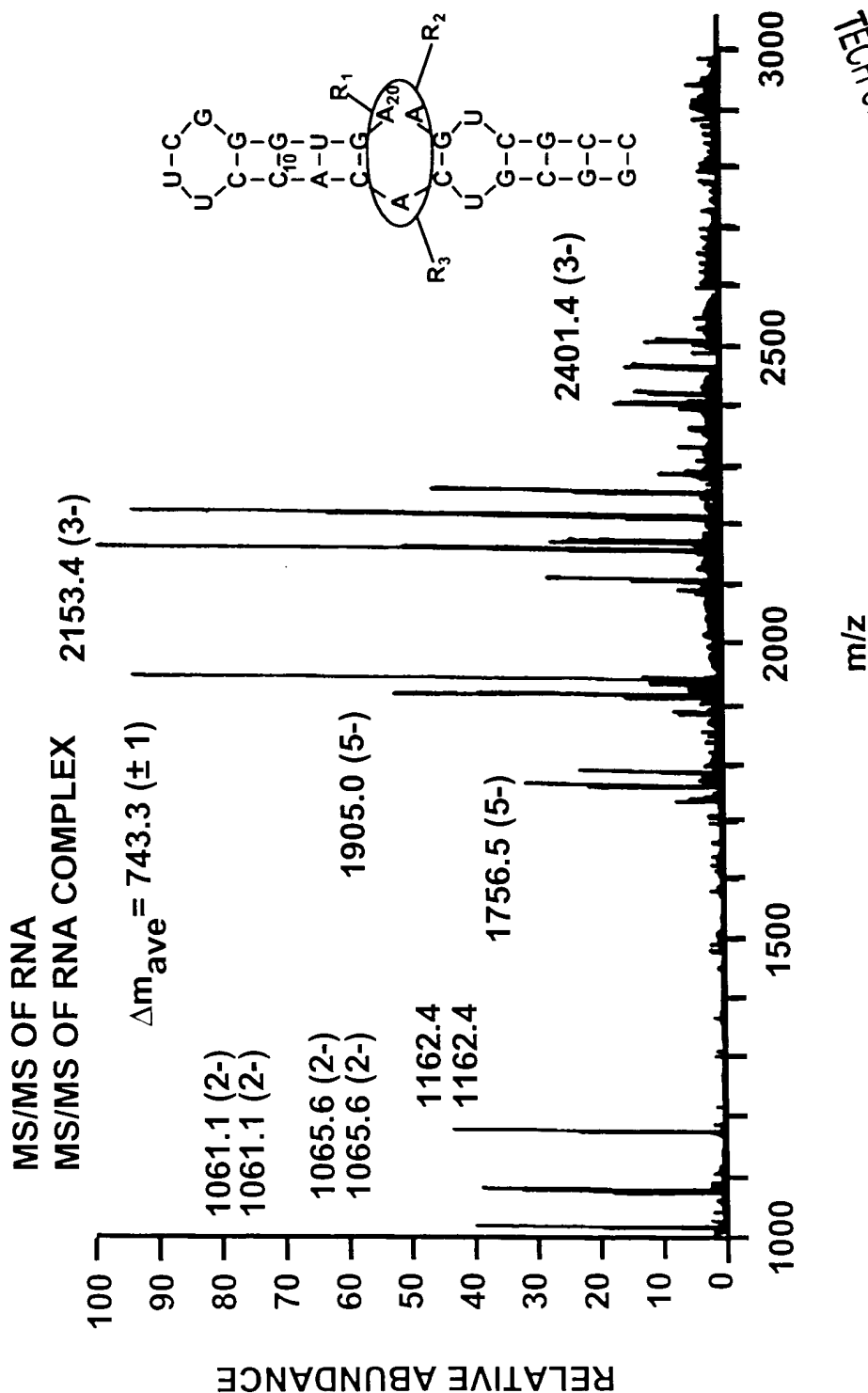


Figure 49



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Figure 50